

Variance and covariance components of Lactation Milk Yield, Body Weight and Calving Interval for Vietnamese purebred Holstein Friesian Cattle under intensive systems

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Abstract

The objective of this study was to estimate the phenotypic, environmental and direct additive and maternal genetic co-variance components of 305-day Milk Yield (MY), Calving Interval (CI) and lactation live Body Weight (BW) traits, with the aim to improve dairy herd through combined multiple trait selection in purebred Holstein Friesian (HF) cattle under intensive system in Vietnam. Data and pedigree records were collected from 5140 purebred HF cows raised in Moc-Chau dairy breeding joint stock company (MC) and Yen-Son cattle development centre, Tuyen-Quang province (TQ), the calving records were gathered from 8 lactations during 1997-2010. MY records in the individuals were collected twice monthly; BW were collected one month after the cows calved, BW of cows were estimated from the technical weight measurement with adjustment of obesity and angularity. CI was calculated from calving records using the consecutive calving days between two successive parities. SAS9.1 and WOMBAT were applied for data analysis and estimating of co-variance components of the traits.

The variance component estimates and their ratios with total phenotypic variances varied in different models. Total heritability for CI varied from 0.07 to 0.09, which is in the low range. Total heritability for BW ranged from 0.22 to 0.34 and for MY from 0.28 to 0.29, in the moderate range of heritability. A negative genetic relationship between the direct additive and maternal additive genetic effects were found for all three traits, CI and BW, from -0.64 to -0.67 for CI and -0.65 for BW; lowly negative genetic relationship for MY, from -0.14 to -0.16. The maternal additive genetic variances as well as maternal heritabilities of CI and MY were negligible and they do not contribute comparatively to selection. The maternal heritabilities were from 0.00 to 0.02 for CI, from 0.02 to 0.05 for MY; maternal heritability of BW varied from 0.02 to 0.26, and may somewhat contribute.

Key words: HF, dairy cattle, CI, BW, MY, heritability, co-variance components, direct additive and maternal effects, permanent environmental effect.

Introduction.

In recent years milk consumption in Vietnam has been surging rapidly, but domestic milk production only meets around 25% of total consumption. Vietnam has to import about 75% of total requirement, and therefore increased milk production has become a substantial need for the nation. In dairy programs purebred Holstein Friesian (HF) cattle are used mainly as nucleus seed stock to breed nucleus bulls and heifers for other local regions. HF cattle are mainly managed in intensive systems. The creation of HF dairy herds with high economic profitability should be an imperative aspiration for Vietnamese dairy farmers. In order to select HF cattle according to farmers' expectation a selection index should include traits such as 305-day milk yield (MY), calving interval (CI) and body weight (BW).

MY is one of the most economically important traits in dairy industry (Brotherstone and Goddard, 2005; Ajili et al., 2007; Thomas and Anilkumar et al., 2009; Hu et al., 2010). Several international researchers reported that the larger cows would give higher milk yield (Clark et al., 1962; Erb et al., 1961; Hooven et al., 1968), but Hansen et al. (1999) showed that it might not be

economically justifiable to continuously select for bigger Holstein cows in North America. Many scientists in the world have shown that dairy cows selected only for higher milk yield would generally show a reduction in fertility (Hoekstra et al., 1994; Grosshans et al., 1997; Royal et al., 2000; Roxstrom et al., 2001; Evans et al., 2002; Royal et al., 2002). Therefore most countries have now begun to combine traits other than those associated with milk production in their selection indexes (Philipsson et al., 1994; Visscher et al., 1994; Bowman et al. 1996; Heringstad et al., 2000; Veerkamp et al., 2002).

CI influences the economic outcome of the dairy enterprise (VanRaden and Klaaskate, 1993; Grohn and Rajala-Schultz, 2000). Longer calving intervals will result in lower economic profitability; gross income is reduced as the result of lower milk production, fewer calves and reduced herd improvement potential. The need for more replacements, veterinary services, medication and repeat services adds to input cost (Pelissier, 1971; Speicher and Meadow., 1967; Louca and Legates., 1967). Because of the antagonistic relationship between MY and CI, cows of high genetic merit for MY have poorer reproductive performance (Pryce et al., 2002).

In this study the heritabilities and other genetic parameters were estimated as a first step to construct a selection index for the improvement of Holstein Frisian cattle in intensive management systems in Vietnam.

Materials and methods

Locations

Data were collected in two intensive Holstein Friesian farms owned by the Moc-Chau joint ventured company, Moc-Chau District, Son-La Province (MC) and the Yen-Son cattle development centre, Yen-Son District, Tuyen-Quang Province (TQ), respectively.

MC is located in an area 1100 meters above sea level. The climate is quite similar to temperate condition, the monthly averaged temperature range from 12-16⁰C in winter to 19-23⁰C in summer, and the average humidity in dry season is about 60-70% and in wet season about 75-80%. The environment and natural conditions are rather favorable to raise dairy cattle.

TQ is located in an area approximately 500 meters above sea level. The climate tends to be of subtropical conditions with monthly average temperature of around 16-20⁰C in winter and 27-30⁰C in summer. The annually averaged humidity is 65-70% in dry season and 80-85% in the wet season.

Data collections

Data were collected from 5140 purebred HF cows raised in MC and TQ, the calving records were gathered from 8 lactations during 1997-2010.

MY records of the individuals were collected twice monthly, the records were combined from morning and afternoon milk records. The time table for morning milking was from 4.00 – 9.00 am, and afternoon milking from 4.00 – 6.00 pm. In MC, almost all dairy farmers use small-sized machines for milking, some farmers still milked their cows by hands, whereas, in TQ, they have milking parlors with quite modern facilities and small-sized machines for milking. The data collections and management were administered by the technical staffs in the company and the centre.

BW was recorded one month after the cows calved. Body weight of cows were estimated from the technical measurement with adjustment of fatness and angularity, and administered by

experienced technical staff. With this method, errors from measurement versus actual weighing were around $\pm 5\%$ that is the acceptable result.

CI was calculated from calving records using the consecutive calving days between two successive parities. The first CI was calculated from two consecutive calving days of first and second parities, and similarly, second CI was calculated from two calving days of second and third parities until seventh CI. If a calving day of a cow was missing the two CI records impacted were not calculated.

Data analyses

Statistical models:

In order to analyze and determine the fixed effect and their significant levels we applied Proc GLM in SAS9.1 with the model as follows as:

$$Y_{ijklmnop} = \mu + \text{Age}_{ijklmnop} + \text{LO}_i + \text{SO}_j + \text{DO}_k + \text{AO}_l + \text{S}_m + \text{L}_n + \text{P}_o + e_{ijklmnop}$$

Where

- $Y_{ijklmnop}$ is calving intervals (days), lactation milk yield (kg), body weight (kg) of p^{th} cow with p^{th} age at calving, reared in i^{th} location, was born from j^{th} sire's origin, k^{th} dam's origin, l^{th} animal's origin, calved in m^{th} season, at n^{th} parity and o^{th} period.
- $\text{Age}_{ijklmnop}$ is age of animals at calving as linear and quadratic regression
- LO_i is the fixed effect of i^{th} locations (LO=2: Moc-Chau company and Yen-Son centre)
- SO_j is the fixed effect of j^{th} Sires' Origins (SO=3: European-American resource, Australia-New Zealand and Asian resource)
- DO_k is the fixed effect of k^{th} Dams' Origins (DO=2: Exotic resource, Domestic resource)
- AO_l is the fixed effect of l^{th} Animals' Origins (AO=2: Exotic resource, Domestic resource)
- S_m is the fixed effect of m^{th} Calvings' seasons (S=2: Winter-Spring (from October through March next year, Summer-Autumn (from April to September))
- L_n is the fixed effect of n^{th} Lactations (L=8: from the first to eighth lactation)
- P_o is the fixed effect of o^{th} calving periods (P=11: Before 2000, 2000, ..., 2008, 2009-2010)
- $e_{ijklmno}$ is random residual with assumed normal distribution $N(0, \sigma_e^2)$

Effects that significantly affect the traits will be fitted in the models to estimating co-variance components. To estimate co-variance components for the three traits, we used WOMBAT (Meyer 2007) from AGBU-UNE with six different models, all of them are repeated record models.

- Model 1: Basic model with only additive genetic effect and animal permanent environment effects fitted.

$$Y = Xb + Z_a u_a + Z_{ape} u_{ape} + e \quad (1)$$

$$\begin{bmatrix} X'X & X'Z_a & X'Z_{ape} \\ Z'_a X & Z'_a Z_a + A^{-1}\lambda_a & Z'_a Z_{ape} \\ Z'_{ape} X & Z'_{ape} Z_a & Z'_{ape} Z_{ape} + I\lambda_{ape} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u}_a \\ \hat{u}_{ape} \end{bmatrix} = \begin{bmatrix} X'Y \\ Z'_a Y \\ Z'_{ape} Y \end{bmatrix}$$

- Model 2: Model 1 + maternal additive genetic effects, but $\sigma_{AM}=0$.

$$Y = Xb + Z_a u_a + Z_m u_m + Z_{ape} u_{ape} + e \quad (2) \text{ with } \sigma_{AM}=0$$

$$\begin{bmatrix} X'X & X'Z_a & X'Z_m & X'Z_{ape} \\ Z'_a X & Z'_a Z_a + A^{-1}\lambda_a & Z'_a Z_m & Z'_a Z_{ape} \\ Z'_m X & Z'_m Z_a & Z'_m Z_m + A^{-1}\lambda_m & Z'_m Z_{ape} \\ Z'_{ape} X & Z'_{ape} Z_a & Z'_{ape} Z_m & Z'_{ape} Z_{ape} + I\lambda_{ape} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u}_a \\ \hat{u}_m \\ \hat{u}_{ape} \end{bmatrix} = \begin{bmatrix} X'Y \\ Z'_a Y \\ Z'_m Y \\ Z'_{ape} Y \end{bmatrix}$$

- Model 3: Model 2 + Covariance direct and maternal additive genetic effects ($\sigma_{AM}\neq 0$).

$$Y = Xb + Z_a u_a + Z_{ape} u_{ape} + Z_m u_m + e \quad (3) \text{ with } \sigma_{AM}\neq 0$$

$$\begin{bmatrix} X'X & X'Z_a & X'Z_m & X'Z_{ape} \\ Z'_a X & Z'_a Z_a + A^{-1}\lambda_a & Z'_a Z_m + A^{-1}\lambda_{am} & Z'_a Z_{ape} \\ Z'_m X & Z'_m Z_a + A^{-1}\lambda_{am} & Z'_m Z_m + A^{-1}\lambda_m & Z'_m Z_{ape} \\ Z'_{ape} X & Z'_{ape} Z_a & Z'_{ape} Z_m & Z'_{ape} Z_{ape} + I\lambda_{ape} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u}_a \\ \hat{u}_m \\ \hat{u}_{ape} \end{bmatrix} = \begin{bmatrix} X'Y \\ Z'_a Y \\ Z'_m Y \\ Z'_{ape} Y \end{bmatrix}$$

- Model 4: Model 1 + maternal permanent environment effects.

$$Y = Xb + Z_a u_a + Z_{ape} u_{ape} + Z_{mpe} u_{mpe} + e \quad (4)$$

$$\begin{bmatrix} X'X & X'Z_a & X'Z_{ape} & X'Z_{mpe} \\ Z'_a X & Z'_a Z_a + A^{-1}\lambda_a & Z'_a Z_{ape} & Z'_a Z_{mpe} \\ Z'_{ape} X & Z'_{ape} Z_a & Z'_{ape} Z_{ape} + I\lambda_{ape} & Z'_{ape} Z_{mpe} \\ Z'_{mpe} X & Z'_{mpe} Z_a & Z'_{mpe} Z_{ape} & Z'_{mpe} Z_{mpe} + I\lambda_{mpe} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u}_a \\ \hat{u}_{ape} \\ \hat{u}_{mpe} \end{bmatrix} = \begin{bmatrix} X'Y \\ Z'_a Y \\ Z'_{ape} Y \\ Z'_{mpe} Y \end{bmatrix}$$

- Model 5: Model 4 + maternal additive genetic effects, and ($\sigma_{AM}=0$).

$$Y = Xb + Z_a u_a + Z_m u_m + Z_{ape} u_{ape} + Z_{mpe} u_{mpe} + e \quad (5) \text{ with } \sigma_{AM}=0$$

$$\begin{bmatrix} X'X & X'Z_a & X'Z_m & X'Z_{ape} & X'Z_{mpe} \\ Z'_a X & Z'_a Z_a + A^{-1}\lambda_a & Z'_a Z_m & Z'_a Z_{ape} & Z'_a Z_{mpe} \\ Z'_m X & Z'_m Z_a & Z'_m Z_m + A^{-1}\lambda_m & Z'_m Z_{ape} & Z'_m Z_{mpe} \\ Z'_{ape} X & Z'_{ape} Z_a & Z'_{ape} Z_m & Z'_{ape} Z_{ape} + I\lambda_{ape} & Z'_{ape} Z_{mpe} \\ Z'_{mpe} X & Z'_{mpe} Z_a & Z'_{mpe} Z_m & Z'_{mpe} Z_{ape} & Z'_{mpe} Z_{mpe} + I\lambda_{mpe} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u}_a \\ \hat{u}_m \\ \hat{u}_{ape} \\ \hat{u}_{mpe} \end{bmatrix} = \begin{bmatrix} X'Y \\ Z'_a Y \\ Z'_m Y \\ Z'_{ape} Y \\ Z'_{mpe} Y \end{bmatrix}$$

- Model 6: Model 5 + Covariance direct and maternal additive genetic effects ($\sigma_{AM} \neq 0$).

$$Y = Xb + Z_a u_a + Z_{ape} u_{ape} + Z_m u_m + Z_{mpe} u_{mpe} + e \quad (6) \text{ with } \sigma_{AM} \neq 0$$

$$\begin{bmatrix} X'X & X'Z_a & X'Z_m & X'Z_{ape} & X'Z_{mpe} \\ Z'_a X & Z'_a Z_a + A^{-1}\lambda_a & Z'_a Z_m + A^{-1}\lambda_{am} & Z'_a Z_{ape} & Z'_a Z_{mpe} \\ Z'_m X & Z'_m Z_a + A^{-1}\lambda_{am} & Z'_m Z_m + A^{-1}\lambda_m & Z'_m Z_{ape} & Z'_m Z_{mpe} \\ Z'_{ape} X & Z'_{ape} Z_a & Z'_{ape} Z_m & Z'_{ape} Z_{ape} + I\lambda_{ape} & Z'_{ape} Z_{mpe} \\ Z'_{mpe} X & Z'_{mpe} Z_a & Z'_{mpe} Z_m & Z'_{mpe} Z_{ape} & Z'_{mpe} Z_{mpe} + I\lambda_{mpe} \end{bmatrix} \begin{bmatrix} \hat{b} \\ \hat{u}_a \\ \hat{u}_m \\ \hat{u}_{ape} \\ \hat{u}_{mpe} \end{bmatrix} = \begin{bmatrix} X'Y \\ Z'_a Y \\ Z'_m Y \\ Z'_{ape} Y \\ Z'_{mpe} Y \end{bmatrix}$$

$$\lambda_a = \frac{\sigma_e^2}{\sigma_a^2}; \lambda_m = \frac{\sigma_e^2}{\sigma_m^2}; \lambda_{ape} = \frac{\sigma_e^2}{\sigma_{ape}^2}; \lambda_{mpe} = \frac{\sigma_e^2}{\sigma_{mpe}^2}; \begin{bmatrix} \lambda_a & \lambda_{am} \\ \lambda_{am} & \lambda_m \end{bmatrix} = \sigma_e^2 \begin{bmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{bmatrix}^{-1} \text{ were applied in Model 3 and}$$

Model 6.

Where

Y is being the vector of N observations for the traits: CI, BW and MY on the animals

X is being $N \times N_f$ incidence matrix of fixed effects

b is being the vector of N_f fixed effects including covariable of age at calving

Z_a is incidence matrix of animals' random direct additive effects

u_a is being the vector of $N \times N_a$ animals' random direct additive effects

Z_m is being incidence matrix of maternal random additive effects

u_m is being the vector of $N \times N_m$ maternal random direct additive effects

Z_{ape} is being incidence matrix of animals' permanent environment effects

u_{ape} is being the vector of $N \times N_{ape}$ animals' permanent environment effects

Z_{mpe} is being incidence matrix of maternal permanent environment effects

u_{mpe} is being the vector of $N \times N_{mpe}$ maternal permanent environment effects

A is numerator relationship matrix

I is identity matrix

e is being the vector of N random residual errors

Likelihood ratio tests were applied to determine the significant levels of the additional components in the different models (Meyer 1989).

Likelihood Ratio (LR) = $-2[\text{Likelihood}(\text{null model}) - \text{Likelihood}(\text{alternative model})]$
 LR will be compared to tabulated Chi-Square value at critical level of 3.84 ($P < 0.05$).

In order to calculate the total genetic variances and the total heritability, the following formulae were applied (Willham, 1972):

$V_G(\text{total}) = V_A + V_M + \text{COV}(A, M)$ in Model 2, Model 3, Model 5 and Model 6.

$$h_T^2 = \frac{V_A + 0.5 * V_M + 1.5 * \text{COV}(A, M)}{V_P}$$

The information about pedigree and records in dataset was shown in Table 1, the descriptive statistical results of CI, BW and MY traits were shown in Table 2. The results of analysis of variance were shown in Table 3. The factors indicated that they affected significantly the traits (CI, BW and MY) with the probabilities levels less than or equal 0.05 ($P \leq 0.05$) would be included in the Models to estimate the genetic, environmental and phenotypic parameters for those traits.

Table 1: Number of animals in pedigree and number of records in dataset

Items	BW	CI	MY
No. of animals with records	3837	4441	5006
No. of animals without offspring	3383	3509	3967
No. of animals with offspring	1122	1575	1756
... and records	454	932	1039
No. of animals with unknown sire	1084	1127	1229
No. of animals with unknown dam	3224	3057	3439
No. of animals with both parents unknown	1040	1063	1148
No. of animals with records			
... and unknown sire	416	484	512
... and unknown dam	2556	2414	2722
... and both parents unknown	372	420	431
No. of sires	396	405	446
No. of dams	726	1170	1310
... with records & progeny in data	454	932	1039
No. of animals with known/unpruned grand-parents			
... with paternal grandsire	0	0	0
... with paternal granddam	0	0	0

... with maternal grandsire	526	1264	1425
... with maternal granddam	265	769	880

Table 2: The basic statistics of three traits

Traits	n	Mean	SD	Min	Max
CI (days)	12500	430.6	72.4	300.0	730.0
BW (kg)	10055	481.1	59.4	260.0	760.0
MY (kg)	14834	4950.8	1106.2	798.0	14746.0

Table 3: Analysis of variances for fixed effects on three traits and determinant coefficients in the models

Traits	Source of Variations	DF	F Value	Pr > F	R ²
CI (Days)	Age(Lactations)	7	6.96	<.0001	0.09
	Regions	1	85.89	<.0001	
	Sire Origin	2	5.53	0.0040	
	Dam Origin	1	8.40	0.0038	
	Animal Origin	1	20.83	<.0001	
	Seasons	1	1.56	0.2116	
	Lactations	6	6.61	<.0001	
BW (Kg)	Periods	10	31.75	<.0001	
	Age*Age	1	0.53	0.4684	0.38
	Regions	1	291.27	<.0001	
	Sire Origin	2	14.93	<.0001	
	Dam Origin	1	17.89	<.0001	
	Animal Origin	1	7.53	0.0061	
	Seasons	1	14.65	0.0001	
Lactations	7	223.3	<.0001		
MY 305 days (Kg)	Periods	10	64.39	<.0001	
	Age*Age	1	61.28	<.0001	0.31
	Regions	1	1232.63	<.0001	
	Sire Origin	2	49.81	<.0001	
	Dam Origin	1	21.35	<.0001	
	Animal Origin	1	12.63	0.0004	
	Seasons	1	5.53	0.0187	
Lactations	7	51.94	<.0001		
Periods	10	97.76	<.0001		

Results and discussions

Co-variances and parameters of Calving Interval.

The results are presented in Table 4. Phenotypic variance estimates for CI varied in different models. Specifically, these estimates were $5109.4 \pm 66.2 \text{ day}^2$, $5107.8 \pm 66.2 \text{ day}^2$, $5115.9 \pm 66.9 \text{ day}^2$, $5109.4 \pm 66.2 \text{ day}^2$, $5107.8 \pm 66.2 \text{ day}^2$, $5168.8 \pm 69.1 \text{ day}^2$, respectively in Model 1, Model 2, Model 3, Model 4, Model 5 and Model 6. In this study, phenotypic variances of CI ranged from 5107.8 day^2 to 5168.8 day^2 , which were much greater than the findings from some other scientists: 883 day^2 from Haile-Mariam et al (2003) in Australian HF herds; 1471.1 day^2 on HF in the Republic of Ireland (Olori et al., 2002); from 1801.0 to 1858.7 day^2 (calculated from components in three first lactations) from Berry et al (2008) in Irish HF cows; but lower than 6466 day^2 on HF herd in Florida (Campos et al., 1994).

Similarly, the direct genetic variance component estimates for this trait were much different in six Models, $437.1 \pm 73.9 \text{ day}^2$, $416.0 \pm 78.3 \text{ day}^2$, $526.2 \pm 117.9 \text{ day}^2$, $437.1 \pm 75.4 \text{ day}^2$, $416.1 \pm 78.3 \text{ day}^2$, $627.2 \pm 135.5 \text{ day}^2$, respectively in Model 1, Model 2, Model 3, Model 4, Model 5, Model 6. These estimates ranged from 416.0 to 627.2 day^2 . The total genetic variance component was estimated to be 437.8, 472.9, 437.8, 558.3 day^2 , respectively in Model 2, Model 3, Model 5 and Model 6. These results were much higher than 53.12 day^2 on HF in the Republic of Ireland (Olori et al., 2002); $82.8 - 136.3 \text{ day}^2$ in South African HF (Makgahlela et al., 2008); but lower than 635 day^2 on HF herd in Florida (Campos et al., 1994).

Otherwise, estimates of other components such as variance estimates of animals' permanent environment component, maternal additive genetic component, covariance between direct and maternal additive genetic component changed with the model fitted.

Maternal additive genetic variance component estimates were $21.8 \pm 37.1 \text{ day}^2$ in Model 2, $66.4 \pm 58.1 \text{ day}^2$ in Model 3, $21.7 \pm 43.0 \text{ day}^2$ in Model 5 and $87.6 \pm 73.6 \text{ day}^2$ in Model 6. So, maternal additive variances varied from 21.7 to 87.6 day^2 . But all these estimates were not significant ($P > 0.05$). These results were much different from negligible values of zero or nearly zero (0.74) of Berry et al. (2008) Covariance between direct and maternal additive genetic components were all negative and attained in Model 6 with the value of $-156.6 \pm 76.9 \text{ day}^2$ ($P > 0.05$), lower than in Model 3 with the value of $-119.7 \pm 66.5 \text{ day}^2$ ($P < 0.05$).

Animals' permanent environment variance component estimates were zero in all models. Maternal permanent environment variance estimates were also zero. The likelihood ratios increased from Model 1 to Model 6, but increment was not much when the additional parameters were fitted.

The direct heritability estimates for CI varied from 0.08 ± 0.02 with Model 2 and Model 5, 0.09 ± 0.01 in Model 1 and Model 4, 0.10 ± 0.02 in Model 3 to the highest value of 0.12 ± 0.03 in Model 6. The total heritabilities were estimated to be 0.09, 0.07, 0.09 and 0.08, respectively in Model 2, Model 3, Model 5 and Model 6. So, in this research, the direct heritability of CI varied from 0.08 ± 0.02 to 0.12 ± 0.03 , and the general heritability ranged from 0.07 to 0.09, which are considered to be in the low range ($h^2 \leq 0.15$). Haile-Mariam et al (2003) reported that heritability of CI on Australian dairy herds was 0.09 ± 0.02 , rather similar to these results. Otherwise, Campos et al. (1994) also reported a similar heritability of Calving Interval (0.10 ± 0.04) to this study. But these results were much higher than the result of 0.04 ± 0.01 reported by Olori et al (2002) on the HF cattle in the Public of Ireland; or 0.02 to 0.03 in three first lactations from Berry et al (2008); 0.03 ± 0.01 on the UK dairy cattle (Banos et al., 2007); the range from 0.03 to

0.04 on South African HF (Makgahlela et al., 2008); 0.04 on the Canadian HF (Dadati et al., 1986).

The estimates of the maternal heritability were 0.00 ± 0.01 , 0.01 ± 0.01 , 0.00 ± 0.01 and 0.02 ± 0.01 , respectively in Model 2, M model 3, Model 5 and Model 6, all of them not statistically significant ($P > 0.05$). As a result, this effect had little influence on the phenotypic component. These results were also similar to Berry et al. (2008) (zero or nearly equal to zero) and 0.01 ± 0.01 (Banos et al., 2007).

Table 4: The variance-covariance components and parameters in the different models applied to analyze CI.

Models (LL)	Parameters	V_G	V_a	V_{am}	V_m	V_{ape}	V_{mpe}	V_e	V_p	LRT
1 (-60784.0)	Co-Variances		437.1			0.01		4672.3	5109.4	0.00
	SE of Var		73.9			68.4		70.7	66.2	
	Ratio		0.09			0.00		0.91		
	SE of Ratio		0.01			0.01		0.01		
2 (-60783.8)	Co-Var	437.8	416.0		21.8	0.00		4670.0	5107.8	0.52 ($P > 0.05$) M1-M2 NS
	SE of Var		78.3		37.1	68.9		70.6	66.2	
	Ratio- h^2_T	0.09	0.08		0.00	0.00		0.91		
	SE of Ratio		0.02		0.01	0.01		0.01		
3 (-60781.1)	Co-Var	472.9	526.2	-119.7	66.4	0.00		4643.0	5115.9	5.41 ($P < 0.05$) M2-M3
	SE of Co-Var		117.9	66.5	58.1	83.6		70.2	66.9	
	Ratio- h^2_T	0.07	0.10		0.01	0.00		0.91		
	SE of Ratio		0.02		0.01	0.02		0.01		
	Correlation			-0.64						
SE of Correlation			0.22							
4 (-60784.0)	Co-Var		437.1			0.01	0.01	4672.3	5109.4	0.00 ($P > 0.05$) M1-M4 (NS)
	SE of Var		75.4			78.8	52.8	70.7	66.2	
	Ratio		0.09			0.00	0.00	0.91		
	SE of Ratio		0.01			0.02	0.01	0.01		
5 (-60783.8)	Co-Var	437.8	416.1		21.7	0.01	0.00	4670.0	5107.8	0.52 ($P > 0.05$) M4-M5 NS
	SE of Var		78.3		43.0	79.5	62.1	70.6	66.2	
	Ratio- h^2_T	0.09	0.08		0.00	0.00	0.00	0.91		
	SE of Ratio		0.02		0.01	0.02	0.01	0.01		
6 (-60782.2)	Co-Var	558.3	627.2	-156.6	87.6	1.9	0.01	4608.6	5168.8	3.14 ($P > 0.05$) M5-M6 NS
	SE of Var		135.5	76.9	73.6	102.6	69.7	69.8	69.1	
	Ratio- h^2_T	0.08	0.12		0.02	0.00	0.00	0.89		
	SE of Ratio		0.03		0.01	0.02	0.01	0.01		
	Correlation			-0.67						
SE of Correlation			0.22							

Where: V_G : total genetic component; V_a : Direct additive genitive component; V_{am} : Covariance component between the direct additive genetic and maternal additive values; V_m : Maternal additive component; V_{ape} : animals' permanent environment component; V_{mpe} : Maternal permanent environment component; V_e : Residual component. V_p : Phenotypic component; LL: Log Likelihood; LRT: Log Likelihood ratio test.

The coefficients of genetic correlation between maternal additive genetic and direct additive genetic effect were -0.64 ± 0.01 in Model 3, and -0.67 ± 0.22 but not significant ($P > 0.05$), indicating the lack of depth in the pedigree with performance data to estimate this parameter. These results were much different from zero value of Berry et al (2008).

The estimates of the ratio animals' permanent environment effect over phenotypic variance were very close to zero in all models. The same can be said for the maternal permanent environmental effect. These results also resemble the findings 0.00 (Berry et al., 2008).

Co-variances and parameters of Body Weight.

The results in Table 5 showed that the phenotypic variance estimates for BW varied little between the six different Models. Specifically, these estimates were $2374.0 \pm 45.9 \text{ kg}^2$, $2363.4 \pm 45.4 \text{ kg}^2$, $2398.6 \pm 49.3 \text{ kg}^2$, $2372.4 \pm 45.8 \text{ kg}^2$, $2369.6 \pm 45.9 \text{ kg}^2$, $2398.6 \pm 49.3 \text{ kg}^2$, respectively in Model 1 to 6. These results were similar to 2492.6 kg^2 on Dutch HF (Koenen and Groen, 1998); but much higher than 1656.49 kg^2 on Quebec HF (Parke et al., 1999).

Direct additive genetic variance component estimates for this trait varied more between the six Models. The largest estimate was the value of $974.4 \pm 154.3 \text{ kg}^2$ in Model 3, and then the value of $974.1 \pm 154.5 \text{ kg}^2$ in Model 6; the moderate values were $788.7 \pm 92.2 \text{ kg}^2$ in Model 1, and then $727.6 \pm 96.0 \text{ kg}^2$ in Model 4 and $703.7 \pm 106.4 \text{ kg}^2$ in Model 5; the lowest estimate was $669.2 \pm 103.7 \text{ kg}^2$ attained in Model 2. The total genetic variance were estimated to be 803.2, 1083.6, 740.4, 1083.5 kg^2 , respectively in Model 2, Model 3, Model 5 and Model 6. These results were similar to 813.7 kg^2 on Dutch Holstein Friesian (Koenen and Groen, 1998).

Maternal additive genetic variance component was fitted in four models and its estimates received the lowest value of $36.7 \pm 89.1 \text{ kg}^2$ in Model 5, the moderate value of $134.0 \pm 103.7 \text{ kg}^2$ in Model 2 and the largest values of $614.4 \pm 225.3 \text{ kg}^2$ in Model 6 and $614.3 \pm 130.7 \text{ day}^2$ in Model 3. However, the estimates were not significant in Model 2 and Model 4 ($P > 0.05$). Covariance between the direct and maternal additive genetic components were all negative and attained the value of -505.1 ± 118.3 in Model 3 and the value of -505.1 ± 134.8 in Model 6.

Animals' permanent environment variance estimates also varied and ranged from 425.2 ± 76.9 ; 399.9 ± 75.2 ; 158.6 ± 100.2 ; 315.3 ± 84.0 ; 327.8 ± 87.1 and $158.8 \pm 103.4 \text{ kg}^2$ in Model 1 to 6, respectively.

Maternal permanent environment variance estimates attained the value of 169.9 ± 69.2 in Model 4 and the value of 141.6 ± 97.3 in Model 5, and the received the value of $0.0 \pm 138.6 \text{ kg}^2$ in Model 6. Both estimates of animals' permanent environment and maternal permanent environment variance components for this trait had got large standard errors.

The likelihood ratios tended to increase from Model 1 to Model 6, but increment were small when the additional parameters were fitted. However, these increments were higher than in CI.

The direct heritability estimates varied in the six Models and were 0.33 ± 0.04 , 0.28 ± 0.04 , 0.41 ± 0.06 , 0.31 ± 0.04 , 0.30 ± 0.04 , 0.41 ± 0.06 in Model 1 to 6, respectively. The total heritabilities were 0.34, 0.22, 0.31 and 0.22 respectively in Model 2, Model 3, Model 5 and Model 6. And thus, the general heritability for BW trait ranged from 0.22 to 0.34, which belongs into the moderate range. These results were also slightly similar to the value of 0.35 on Quebec Holstein Friesian cattle (Parke et al., 1999); 0.33 on Dutch HF (Koenen and Groen, 1998); but much lower than 0.60 ± 0.08 on HF of Pennsylvania (Vallimont et al., 2010).

The estimates of maternal additive genetic effect were smaller in Model 2 and Model 5 (0.06 ± 0.03 , 0.02 ± 0.04), and much larger in Model 3 and Model 6 (0.26 ± 0.05 and 0.26 ± 0.09), respectively. The estimates in Model 2 and Model 5 were not statistically significant ($P>0.05$).

The correlation coefficients between maternal additive genetic and direct additive genetic effects were quite large and negative (-0.65 ± 0.08). The results indicated that for BW trait in these herds, when one is interested in selecting animals with high values of the direct additive genetic breeding values, it would reduce the maternal additive genetic breeding values in those animals and their progeny.

Table 5: The variance-covariance components and parameters in the different models applied to analyze BW.

Models (LL)	Parameters	V_G	V_a	V_{am}	V_m	V_{ape}	V_{mpe}	V_e	V_p	LRT
1 (-42704.1)	Var		788.7			425.2		1160.2	2374.0	0.00
	SE of Var		92.2			76.9		21.0	45.9	
	Ratio		0.33			0.18		0.49		
	SE of Ratio		0.04			0.03		0.01		
2 (-42702.4)	Var	803.2	669.2		134.0	399.9		1160.3	2363.4	3.51 (M1-M2) NS
	SE of Var		103.7		69.8	75.2		21.0	45.4	
	Ratio- h^2_T	0.34	0.28		0.06	0.17		0.49		
	Seof Ratio		0.04		0.03	0.03		0.01		
3 (-42689.3)	Var	1083.6	974.4	-505.1	614.3	158.6		1156.4	2398.6	26.03 (M2-M3)
	SE of Var		154.3	118.3	130.7	100.2		21.0	49.3	
	Ratio- h^2_T	0.22	0.41		0.26	0.07		0.48		
	SE of Ratio		0.06		0.05	0.04		0.01		
	Correlation			-0.65						
SE of Correl			0.08							
4 (-42701.6)	Var		727.6			315.3	169.9	1159.6	2372.4	5.08 (M1-M4)
	SE of Var		96.0			84.0	69.2	21.0	45.8	
	Ratio		0.31			0.13	0.07	0.49		
	SE of Ratio		0.04			0.04	0.03	0.01		
5 (-42701.5)	Var	740.4	703.7		36.7	327.8	141.6	1159.7	2369.6	0.21 (M4-M5) NS
	SE of Var		106.4		89.1	87.1	97.3	21.0	45.9	
	Ratio- h^2_T	0.31	0.30		0.02	0.14	0.06	0.49		
	SE of Ratio		0.04		0.04	0.04	0.04	0.01		
6 (-42689.3)	Var	1083.5	974.1	-505.1	614.4	158.8	0.000	1156.3	2398.6	24.25 (M5-M6)
	SE of Var		154.5	134.8	225.3	103.4	138.6	21.0	49.3	
	Ratio- h^2_T	0.22	0.41		0.26	0.07	0.00	0.48		
	SE of Ratio		0.06		0.09	0.04	0.06	0.01		
	Correlation			-0.65						
SE of Correl			0.08							

Where: V_G : total genetic component; V_a : Direct additive genitive component; V_{am} : Covariance component between the direct additive genetic and maternal additive values; V_m : Maternal additive component; V_{ape} : animals' permanent environment component; V_{mpe} : Maternal permanent environment component; V_e : Residual component. V_p : Phenotypic component; LL: Log Likelihood; LRT: Log Likelihood ratio test.

The estimates of animals' permanent environment effect were estimated to be large in three Models: 0.18 ± 0.03 in Model 1, 0.17 ± 0.03 in Model 2, 0.13 ± 0.04 in Model 4 and 0.14 ± 0.04 in Model 5; and estimated to be smaller values: 0.07 ± 0.04 in Model 3 and 0.07 ± 0.04 in Model 6,

because in these two Models, the additive genetic covariance between direct and maternal components was fitted and then the components were changed and compensated among them. The results indicated that animals' permanent environment effect was considerable and plays an important role.

The estimates of maternal permanent environment effect were 0.07 ± 0.03 , 0.06 ± 0.04 , 0.00 ± 0.06 , respectively in Model 4, Model 5 and Model 6. The estimate received the value of zero in Model 6, it may be the additive genetic covariance. Nonetheless, this effect also plays the definite role in the improvement of the trait.

Co-variances and parameters of Milk Yield.

The results are presented in Table 6. Phenotypic variance component estimates for MY were similar for all six Models. Specifically, these estimates were $865838.0 \pm 13383.2 \text{ kg}^2$, $862369.0 \pm 13306.6 \text{ kg}^2$, $864523.0 \pm 13713.0 \text{ kg}^2$, $864855.0 \pm 13398.1 \text{ kg}^2$, $863575.0 \pm 13396.2 \text{ kg}^2$ and $865426.0 \pm 13795.7 \text{ kg}^2$, respectively in Model 1 to 6. So, the phenotypic variances of MY in this research ranged from $862369.0 \pm 13306.6 \text{ kg}^2$ to $865838.0 \pm 13383.2 \text{ kg}^2$.

The direct additive genetic variance component estimates for this trait differed slightly among the six Models. These estimates were $251835 \pm 23520.6 \text{ kg}^2$, $218117.0 \pm 27267.8 \text{ kg}^2$, $237425.0 \pm 38864.2 \text{ kg}^2$, $239964.0 \pm 24395.5 \text{ kg}^2$, $229190.0 \pm 27231.7 \text{ kg}^2$ and $245842.0 \pm 39372.7 \text{ kg}^2$, respectively in Model 1 to 6. The total genetic variance was estimated to be 251486.7 , 264129.3 , 242924.4 , 253163.8 kg^2 , respectively in Model 2, Model 3, Model 5 and Model 6.

Estimates of other components such as variance estimates of animals' permanent environment component, maternal additive genetic component, covariance between direct and maternal additive genetic component changed in the fitted models.

Maternal additive genetic variance component estimates in this research received the values of $33369.7 \pm 15568.6 \text{ kg}^2$ in Model 2, $40165.7 \pm 20328.0 \text{ kg}^2$ in Model 3, $13734.4 \pm 17107.6 \text{ kg}^2$ in Model 5 and $17758.6 \pm 20348.8 \text{ kg}^2$ in Model 6. However, the estimate received in Model 2 was not significant ($P > 0.05$). Covariance between direct and maternal additive genetic components were both negative, and -10436.8 ± 19593.2 in Model 6 and larger in Model 3 -13461.4 ± 21060.2 , but both the estimates were not statistically significance ($P > 0.05$).

Animals' permanent environment variance component estimates also varied and ranged from 122709.0 ± 18158.1 ; 119511.0 ± 18074.1 ; 109061.0 ± 23650.7 ; 97793.2 ± 20159.1 ; 103258.0 ± 20924.3 and 94956.8 ± 20348.8 in Model 1 to 6, respectively.

Maternal permanent environment variance estimates were 35771.1 ± 14313.1 ; 26039.0 ± 6919.8 and 25979.7 ± 18300.0 in Model 4 to 6, respectively. These estimates were much larger than the range from 0 to 3380.26 kg^2 reported by Berry et al., 2008. Generally, both estimates of animals' permanent environment and maternal permanent environment variance components were estimated with large standard errors.

The likelihood ratios tended increased from Model 1 to Model 6, but increment was not much when the additional parameters were added.

The direct heritability estimates for this trait were various in six Models; 0.29 ± 0.03 ; 0.25 ± 0.03 ; 0.28 ± 0.04 ; 0.28 ± 0.03 ; 0.27 ± 0.03 ; 0.28 ± 0.04 , respectively in Model 1 to 6. The total heritability estimates were 0.29, 0.28, 0.28, 0.28 respectively in Model 2, Model 3, Model 5 and Model 6. And thus, general heritability for MY ranged from 0.28 to 0.29, which is in moderate range.

The estimates of maternal additive genetic effect were quite small and also various in the fitted Models. Two estimates received from Model 2 (0.04 ± 0.02) and Model 3 (0.05 ± 0.02) were bigger than two other estimates from Model 5 (0.02 ± 0.02) and Model 6 (0.02 ± 0.02). These changes may come from fitting the additional component of maternal permanent environment effect in the Models. However, the estimate from Model 5 was not significant ($P > 0.05$).

The correlation coefficients between maternal additive genetic and direct additive genetic effects were -0.14 ± 0.19 and -0.16 ± 0.26 in Model 3 and Model 6, respectively; both were not statistically significant ($P > 0.05$).

The estimates of animals' permanent environment effect were 0.14 ± 0.02 , 0.14 ± 0.02 , 0.13 ± 0.03 , 0.11 ± 0.02 , 0.12 ± 0.03 , 0.11 ± 0.03 , respectively in six Models. These results apparently showed that this effect affected considerably the variation of MY trait contributing to a high repeatability of MY.

The estimates of maternal permanent environment effect were 0.04 ± 0.02 , 0.03 ± 0.02 , 0.03 ± 0.02 respectively in Model 4, Model 5 and Model 6. These estimates were quite low but they showed that the maternal permanent environment effect was important enough to be mentioned in the HF breeding.

In our study, the phenotypic variances of MY in this research ranged from $862369.0 \pm 13306.6 \text{ kg}^2$ to $865838.0 \pm 13383.2 \text{ kg}^2$, which were much higher than 603729 kg^2 on HF in Quebec-Canada (Parke et al., 1999); 693020 kg^2 on HF in Republic of Ireland (Olori et al., 2002). But these estimates were lower than 1071527 kg^2 on HF in Pennsylvania (Campos et al., 1994); 1039704 to 1160952 kg^2 on the Egyptian HF (Adel et al., 2005); and half of the values (1724000 to 1730000 kg^2) reported by Albuquerque et al (1998) in New York HF herd, the main reason was that population mean in that herd ($9022 \text{ kg}/\text{cow}/\text{lactation}$) was almost twice that in this study. Especially, these results were very much lower than 2292447 to 2314464 kg^2 on the HF breeding research herd in Iowa State University (Schutz et al., 1992).

The direct additive genetic variance in this study was considerably fluctuating in the different fitted model and ranged from $218117.0 \pm 27267.8 \text{ kg}^2$ to $251835 \pm 23520.6 \text{ kg}^2$, which was quite similar to the range from 213323.9 to 265142.6 kg^2 on three first lactation of HF in Republic of Ireland (Berry et al., 2008); 255735 to 243686 kg^2 on the Egyptian HF (Adel et al., 2005); but much lower than the range from 323483 to 583040 kg^2 on the HF breeding research herd at Iowa State University (Schutz et al., 1992). Besides, the genetic variance estimates from this study (242924.4 to 253163.8 kg^2) were similar to 275520 kg^2 on HF in Republic of Ireland (Olori et al., 2002); but much lower than 366634 kg^2 on HF in Pennsylvania-USA (Campos et al., 1994).

And thus, the above variance components depended on the characteristics of populations, structures of herds and production categories. Further, they are also affected by the method applied in the analysis.

In these results, the direct heritability estimates ranged from 0.25 ± 0.03 to 0.29 ± 0.03 , in the moderate range of heritability. These estimates were a bit lower than the range from 0.278 to 0.33 in New York HF herd (Albuquerque et al., 1998); from 0.23 to 0.34 on the Irish HF (Berry et al., 2008). But these estimates were higher than the range from 0.22 to 0.23 on the Egyptian HF (Adel et al., 2005); the range from 0.14 to 0.25 , on the HF breeding research herd at Iowa State University (Schutz et al., 1992). Further the estimates of heritability in this study were lower than the results from 0.31 from Parke et al. (1999); 0.34 from Campos et al. (1994); but much lower than 0.56 from Olori et al. (2002).

Otherwise, the results in this study showed that the animals' permanent environment effect also considerably contributed into the phenotypic variance, the estimates of ratio for this effect

ranged from 0.11 ± 0.03 to 0.14 ± 0.02 , which was much lower than the values of 0.24 to 0.25 reported by Albuquerque et al (1998) in New York cow herd; 0.32 to 0.35 reported by Schutz et al. (1992) on HF in Iowa-USA. Banos et al (2007) reported for the UK dairy cattle that the direct heritability was 0.27 ± 0.02 , which was in the range of this study. Adel et al (2005) reported for Egyptian HF that the animals' permanent environment effect ranged from 0.06 to 0.13, which was a bit lower than ours.

The maternal heritability estimates in our study were negligible or small, and ranged from 0.02 to 0.05. This component has little influence on the phenotypic variance. However, it should be interesting to study. Some other scientists also reported that the maternal heritability estimates were small or negligible: from 0.01 (Albuquerque et al., 1998); 0.01 (Adel et al., 2005); 0.05 Lee et al (2003) reported on the Korean HF; 0.00 to 0.01 on the Irish HF (Berry et al., 2008); 0.00 to 0.03 on the HF breeding research herd at Iowa State University (Schutz et al., 1992); 0.00 for the UK dairy cattle (Banos et al., 2007). In similarity, the maternal permanent environment effect in this study was also little and negligible (0.03 ± 0.02 to 0.04 ± 0.02). Berry et al. (2008) also reported small estimates of this effect (0.00 to 0.00) on the Irish HF. The negative and considerable relationship between the direct and maternal effect was reported in this study (-0.14 ± 0.19 and -0.16 ± 0.26) which is unimportant. Other researchers also reported the negative relationship between them: -0.45 (Adel et al., 2005); -0.45 (Lee et al., 2003); -0.46 (Berry et al., 2008). As opposed to this study, and as well as some other results, Albuquerque et al (1998) reported the positive relationship between them.

Conclusions

The variance component estimates and their ratios with total phenotypic variances always varied with different models. It seemed that Model 1 is the best type for data analyses, the parameters from this Model seemed to be proper for application in dairy cattle breeding program.

Total heritability for CI varied from 0.07 to 0.09, which is in the low range. Total heritability for BW ranged from 0.22 to 0.34 and for MY from 0.28 to 0.29, which are in the moderate range of heritability.

The negative genetic relationship between the direct additive and maternal additive genetic effects were found in all three traits, considerably negative relationship found in CI and BW traits, from -0.64 to -0.67 for CI trait and -0.65 for BW trait; lowly negative genetic relationship found in MY trait, from -0.14 to -0.16. The maternal additive genetic variances as well as maternal heritabilities of CI and MY were quite negligible or nearly equal to zero, and they did not contribute comparatively into selection. The maternal heritabilities were from 0.00 to 0.02 for CI, from 0.02 to 0.05 for MY; maternal heritability of BW varied from 0.02 to 0.26, it may somewhat contribute to selection for BW.

The animals' permanent environment variances in BW and MY trait contribute much to their phenotypic variances, whereas the contribution of this component was very low and negligible for CI trait. The animals' permanent environment effect was nearly zeroed for CI, whereas, this effect was from 0.07 to 0.18 for BW and from 0.11 to 0.14 for MY.

With a direct heritability from 0.08 to 0.12 for CI genetic improvement in this trait will be slow and not very efficient. The heritability of BW ranged from 0.28 to 0.41, which was in the moderate to high range; and the heritability of MY ranged from 0.25 to 0.29, which was in the moderate range. It is possible to improve BW and MY traits through genetic improvement.

Table 6: The variance-covariance components and parameters in the different models applied to analyze MY.

Models (LL)	Parameters	V_G	V_a	V_{am}	V_m	V_{ape}	V_{mpe}	V_e	V_p	LRT
1 (-73044.38)	Co-Var		251835			122709.0		491294.0	865838.0	0.00
	SE of Var		23520.6			18158.1		6919.1	13383.2	
	Ratio		0.29			0.14		0.57		
	SE of Ratio		0.03			0.02		0.01		
2 (-73041.67)	Co-Var	251486.7	218117.0		33369.7	119511.0		491372.0	862369.0	5.41 (M1-M2)
	SE of Var		27267.8		15568.6	18074.1		6920.4	13306.6	
	Ratio- h^2_T	0.29	0.25		0.04	0.14		0.57		
	SE of Ratio		0.03		0.02	0.02		0.01		
3 (-73041.49)	Co-Var	264129.3	237425.0	-13461.4	40165.7	109061.0		491333.0	864523.0	0.36 (M2-M3) NS
	SE of Var		38864.2	21060.2	20328.0	23650.7		6919.7	13713.0	
	Ratio- h^2_T	0.28	0.28		0.05	0.13		0.57		
	SE of Ratio		0.04		0.02	0.03		0.01		
	Correlation			-0.14						
	SEof Correl			0.19						
4 (-73041.09)	Co-Var		239964.0			97793.2	35771.1	491327.0	864855.0	6.59 (M1-M4)
	SE of Var		24395.5			20159.1	14313.1	6919.3	13398.1	
	Ratio		0.28			0.11	0.04	0.57		
	SE of Ratio		0.03			0.02	0.02	0.01		
5 (-73040.72)	Co-Var	242924.4	229190.0		13734.4	103258.0	26039.0	491353.0	863575.0	0.72 (M4-M5) NS
	SE of Var		27231.7		17107.6	20924.3	18003.8	6919.8	13396.2	
	Ratio- h^2_T	0.28	0.27		0.02	0.12	0.03	0.57		
	SE of Ratio		0.03		0.02	0.03	0.02	0.01		
6 (-73040.60)	Co-Var	253163.8	245842.0	-10436.8	17758.6	94956.8	25979.7	491325.0	865426.0	0.25 (M5-M6) NS
	SE of Var		39372.7	19593.2	20348.8	25487.9	18300.0	6919.3	13795.7	
	Ratio- h^2_T	0.28	0.28		0.02	0.11	0.03	0.57		
	SE of Ratio		0.04		0.02	0.03	0.02	0.01		
	Correlation			-0.16						
	SEof Correl			0.26						

Where: V_G : total genetic component; V_a : Direct additive genitive component; V_{am} : Covariance component between the direct additive genetic and maternal additive values; V_m : Maternal additive component; V_{ape} : animals' permanent environment component; V_{mpe} : Maternal permanent environment component; V_e : Residual component. V_p : Phenotypic component; LL: Log Likelihood; LRT: Log Likelihood ratio test.

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